

AMENDMENTS TO THE SPECIFICATION

Please replace paragraph [0028] with the following replacement paragraph.

[0028] Figure 9 shows the comparison of the promoters at TATA box regions of resistant (IBB31) (SEQ ID NO:53) and susceptible (IR24) (SEQ ID NO:54) alleles of the *Xa31* gene.

Please replace paragraph [0068] with the following replacement paragraph.

[0068] Since the genomic sequence of chromosome 6 of *O. sativa* cv. Nipponbare was accessible from RGP website and both AM1-TAIL and AM2-TAIL are single copy in rice genome, we then performed fine mapping of the *Xa31* locus by landing the two markers on rice genomic sequence. Firstly, we used the two markers to BLAST the Unfinished High Throughput Genomic Sequences (htgs) of rice (<http://www.ncbi.nlm.nih.gov/blast/index.html>). AM1-TAIL could hit the sequence of AP003615 of RGP PAC clone P0486H12 from chromosome 6 (Identities = 999/1008 (99%) for position 19-1026 on AM1-TAIL). AM2-TAIL picked up the sequences of AP004571 (RGP PAC clone P0652A05), AP004327 (Monsanto BAC clone OJ1378_E04), AP003941 (Monsanto BAC clone OJ1111_E06) and AP003617 (RGP PAC clone P0502H06) (Identities = 412/416 (99%) for position 161-575 and 462/494 (93%) for position 589-1081 on AM2-TAIL). Sequence analysis indicated that the latter four BAC or PAC clones are overlapping clones at the AM2-TAIL locus on chromosome 6 (data not shown). Then we downloaded the genomic sequence as well as genetic markers flanked by AM1-TAIL and AM2-TAIL from RGP website. A genetic map and a physical BAC/PAC contig of the *Xa31* locus were generated as shown in Figure 4A. The physical size between AM1-TAIL and AM2-TAIL was 480-kb on the RGP BAC/PAC contig. To confirm the genetic map, an RGP marker, R674 (kindly provided by T. Sasaki of RGP), was selected for linkage analysis. Two mapping populations, one containing 32 resistant BC4F1 individuals and another 37

resistant BC2F2 individuals including three AM2-TAIL recombinants, were used for RFLP analysis. Hybridization results indicated that the resistance-associated allele of R674 always co-segregated with the resistance individuals except for the three recombinants shared with AM2-TAIL. Linkage analysis with RM2 and AM2-TAIL recombinants also showed that 19 recombinants were located at R674 locus, among which 17 recombinants were shared with AM2-TAIL and two more crossovers (recombinants) occurred within the 20-kb (RGP physical distance) region between R674 and AM2-TAIL.

Please replace paragraph [0086] with the following replacement paragraph.

[0086] BLASTP (<http://www.ncbi.nlm.nih.gov/blast/index.html>) searches showed that no putative conserved domains have been detected within the 113AA (SEQ ID NO: 5). The only similarity found was that the 113 amino acid sequence of SEQ ID NO:5 shows 36.8% or 38.2% of identity at its C-terminal (62-113) to the signal and propeptide regions of rat or human neuroendocrine convertase 1 (NEC1) precursor (EC3.4.21.93) (data not shown).

Please replace paragraph [0099] with the following replacement paragraph.

[0099] DNA sequence analysis. The publicly available BAC (Bacterial Artificial Chromosome) or PAC (P1 Artificial Chromosome, Baba et al. 2000) sequences of *O. sativa* cv. Nipponbare were downloaded from Rice Genome Sequence Program (RGP) website (<http://rgp.dna.affrc.go.jp/cgi-bin/statusdb/stattable.pl?chr=6&lab=RGP> <http://rgp.dna.affrc.go.jp/cgi-bin/statusdb/stattable.pl?chr=6&lab=RGP>) as well as from other available Genbank. DNA sequence was aligned and analyzed using Sequencher 3.0 program. Sequence alignment was also carried out using Pairwise BLAST (<http://www.ncbi.nlm.nih.gov/blast/bl2seq/bl2.html>).